

Amendments to the Claims:

1.-40. (Cancelled)

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41. (Currently amended) A method for the remediation of soil or fluid ~~water~~ contaminated with uranium, comprising contacting soil or ~~water~~ fluid contaminated with uranium with ~~the of transgenic plants as claimed in claim 31~~ a reagent comprising a polypeptide, said polypeptide comprising one or more variants of the calmodulin loop of SEQ ID NO: 13, 14, 15 or 16, wherein the calmodulin loop variant comprises the mutation to neutral residues selected from the group consisting of Serine, Threonine, Cysteine, Histidine, Tyrosine, Asparagine and Glutamine of one or more residues selected from the Aspartic acid residues at positions 1 and 3 of SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15 and SEQ ID NO: 16 and the Aspartic acid residue at position 5 of SEQ ID NO: 13 and SEQ ID NO: 16, and wherein said calmodulin loop variant is flanked at both ends by an alpha helix.

42. (New) The method according to claim 41, wherein said calmodulin loop variant comprises one or more mutations selected from the group consisting of:

- the mutation of the Aspartic acid residue at position 1, 3 or 5 of SEQ ID NO: 13 to a Threonine residue,
- the mutations of the Aspartic acid residues at positions 1 and 5, 1 and 3 or 3 and 5 of SEQ ID NO: 13 to a Threonine, Serine or Asparagine residue,
- the mutations of the Aspartic acid residues at positions 1, 3 and 5 of SEQ ID NO: 13 to a Threonine, Serine or Asparagine residue.

43. (New) The method according to claim 41, wherein both said alpha helices flanking the calmodulin loop variant are from a helix-loop-helix motif of a protein selected from the group consisting of : calmodulin, troponin C, parvalbumin, calbindin, recoverin, neurocalcin, calpain, oncomodulin, sarcoplasmic calcium binding protein, S100 protein, V1S protein and myosin.

44. (New) The method according to claim 43, wherein said both alpha helices are selected from the group consisting of: the sequences SEQ ID NO: 17 and 18, the sequences the

sequences SEQ ID NO: 19 and 20, the sequences SEQ ID NO: 21 and 22, and the sequences SEQ ID NO: 23 and 24.

45. (New) The method according to claim 41, wherein said polypeptide is a cyclic polypeptide in which both said alpha helices flanking the calmodulin loop variant comprise a residue that allows chemical bridging.

46. (New) The method according to claim 45, wherein both said residues are Cysteines which are further connected via a disulfide bridge.

47. (New) The method according to claim 44, wherein said alpha helices of SEQ ID NO: 17 and 18 further comprise the substitution of the Phenylalanine residue at position 13 of SEQ ID NO: 17 and of the Valine residue at positions 4 of SEQ ID NO: 18 to Cysteine residues.

48. (New) The method according to claim 41, wherein said polypeptide comprises a sequence selected from the group consisting of the sequences SEQ ID NO: 4 to 7 and SEQ ID NO: 9 to 12.

49. (New) The method according to claim 41, wherein said polypeptide comprises at least two identical or different calmodulin loop variants flanked at both ends by an alpha helix.

50. (New) The method according to claim 41, wherein said polypeptide is further fused with another protein.

51. (New) The method according to claim 50, wherein said protein is selected from the group consisting of: calmodulin, troponin C, parvalbumin, calbindin, recoverin, neurocalcin, calpain, oncomodulin, sarcoplasmic calcium binding protein, S100 protein, V1S protein and myosin.

52. (New) The method according to claim 41, wherein said reagent further comprises an expression system for said polypeptide, wherein said expression system is a prokaryotic or eukaryotic cell genetically modified with a recombinant vector encoding said polypeptide.

53. (New) The method according to claim 41, wherein said reagent further comprises an expression system for said polypeptide, wherein said expression system is a transgenic plant comprising cells modified with a nucleic acid molecule encoding said polypeptide.

54. (New) The method according to claim 41, wherein said fluid is selected from the group consisting of water and a biological medium.

55. (New) A method for the detection of uranium in the environment or an individual, comprising:

- contacting soil or fluid with a reagent comprising a polypeptide, said polypeptide comprising one or more variants of the calmodulin loop of SEQ ID NO: 13, 14, 15 or 16, wherein the calmodulin loop variant comprises the mutation to neutral residues selected from the group consisting of Serine, Threonine, Cysteine, Histidine, Tyrosine, Asparagine and Glutamine of one or more residues selected from the Aspartic acid residues at positions 1 and 3 of SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15 and SEQ ID NO: 16 and the Aspartic acid residue at position 5 of SEQ ID NO: 13 and SEQ ID NO: 16, and wherein said calmodulin loop variant is flanked at both ends by an alpha helix, and

- detecting said polypeptide which is bound to uranium.

56. (New) The method according to claim 55, wherein said both alpha helices are selected from the group consisting of: the sequences SEQ ID NO: 17 and 18, the sequences the sequences SEQ ID NO: 19 and 20, the sequences SEQ ID NO: 21 and 22, and the sequences SEQ ID NO: 23 and 24.

57. (New) The method according to claim 55, wherein said polypeptide comprises a fluorescent amino acid residue.

58. (New) The method according to claim 55, wherein said fluorescent amino acid residue is a tyrosine residue or a tryptophan residue.

59. (New) The method according to claim 56, wherein the sequences SEQ ID NO: 13

and 17 further comprise an amino acid substitution selected from the group consisting of: the substitution of the Alanine residue at position 9 of SEQ ID NO: 17 to a Tryptophan residue, the substitution of the Phenylalanine residue at position 10 of SEQ ID NO: 17 to a Tryptophan residue, and the substitution of the Threonine residue at position 7 of SEQ ID NO: 13 to a Tyrosine or a Tryptophan residue.

60. (New) The method according to claim 55, wherein said polypeptide comprises a sequence selected from the group consisting of the sequences SEQ ID NO: 4 to 7 and SEQ ID NO: 9 to 12.

61. (New) The method according to claim 55, wherein said polypeptide is conjugated to one or more fluorophores.

62. (New) The method according to claim 61, wherein said fluorophore is a fluorescent protein selected from the group consisting of: EBFP, ECFP, EYFP, EGFP, DsRed, CopGFP and PhiYFP.

63. (New) The method according to claim 61, wherein said fluorophore is selected from the group consisting of: dansyl, coumarin, fluorescein and Alexa derivatives.

64. (New) The method according to claim 61, wherein said polypeptide is conjugated, at one end with a fluorescence donor, and the other end with a fluorescence acceptor.

65. (New) The method according to claim 64, wherein said polypeptide is conjugated, at one end with the EBFP or ECFP protein and at the other end with the EGFP or EYFP protein.

66. (New) The method according to claim 55, wherein said fluid is water or a biological medium.

67. (New) A method for treating individuals contaminated with uranium, comprising administering to an individual contaminated with uranium a polypeptide comprising one or more variants of the calmodulin loop of SEQ ID NO: 13, 14, 15 or 16, wherein the calmodulin loop

variant comprises the mutation to neutral residues selected from the group consisting of Serine, Threonine, Cysteine, Histidine, Tyrosine, Asparagine and Glutamine of one or more residues selected from the Aspartic acid residues at positions 1 and 3 of SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15 and SEQ ID NO: 16 and the Aspartic acid residue at position 5 of SEQ ID NO: 13 and SEQ ID NO: 16, and wherein said calmodulin loop variant is flanked at both ends by an alpha helix.

68. (New) The method according to claim 67, wherein said polypeptide is further associated with at least one molecule which targets the polypeptide to the kidney or the bone or both.

69. (New) The method according to claim 67, wherein said polypeptide is further associated with a molecule that promotes its *in vivo* excretion.